## AMENDMENTS TO THE CLAIMS

1.    (original)    A method for determining whether a candidate cell is a neuro-endocrine tumor cell, wherein said method comprises the steps of:

(A) determining the profile of expression of a plurality of genes of said candidate cell; and

(B) comparing such determined profile of expression with the profile of expression of said genes of a small cell lung cancer cell, a large cell neuroendocrine carcinoma cell, a typical carcinoid tumor cell or an atypical carcinoid tumor cell;

to thereby determine whether said candidate cell is a neuroendocrine tumor cell.

2.    (original)    The method of claim 1, wherein said method additionally permits a determination of neuroendocrine tumor cell type.

3.    (original)    The method of claim 2, wherein said method determines whether said candidate cell is a small cell lung cancer (SCLC) neuroendocrine tumor cell.

4.    (original)    The method of claim 1, wherein said plurality of genes includes one or more genes selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGD1A, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF11, DDX28, DHCR7, ERP70, FEN1, GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCR1, SIP2-28, SIVA, SURF1, TADA3L, TK1, TYMSTR, and VAT1.

5.    (original)    The method of claim 4, wherein said plurality of genes includes one or more genes selected from the group consisting of GGH and CPE.

6.    (original)    The method of claim 2, wherein said method determines whether said candidate cell is a large cell neuroendocrine carcinoma (LCNEC)

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neuroendocrine tumor cell.

7.    (original)    The method of claim 2, wherein said method determines whether said candidate cell is a typical carcinoid (TC) neuroendocrine tumor cell.

8.    (original)    The method of claim 2, wherein said method determines whether said candidate cell is an atypical carcinoid (AC) neuroendocrine tumor cell.

9.    (original)    The method of claim 2, wherein said step (A) comprises incubating RNA of said candidate cell, or DNA or RNA amplified from such RNA, in the presence of a plurality of genes, or fragments or RNA transcripts thereof, under conditions sufficient to cause RNA to hybridize to complementary DNA or RNA molecules; and detecting hybridization that occurs.

10.    (original)    The method of claim 9, wherein said plurality of genes, or polynucleotide fragments or RNA transcripts thereof, are distinguishably arrayed in a microarray.

11.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in-neuroendocrine tumor cells relative to normal cells.

12.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells.

13.    (original)    The method of claim 12, wherein said arrayed genes, or polynucleotide fragments or RNA transcripts thereof, include one or more genes selected

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from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGD1A, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1, GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCRI, SIP2-28, SIVA, SURF 1, TADA3L, TK1, TYMSTR, and VATI, or a polynucleotide fragment or RNA transcript thereof.

14.    (original)    The method of claim 13, wherein said arrayed genes, or polynucleotide fragments or RNA transcripts thereof, includes one or more genes selected from the group consisting of GGH and CPE, or a polynucleotide fragment or RNA transcript thereof.

15.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to typical carcinoid (TC) neuroendocrine tumor cells.

16.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

17.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells relative to typical carcinoid (TC) neuroendocrine tumor cells.

18.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are

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differentially expressed in large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

19.    (original)    The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in typical carcinoid (TC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

20.    (original)    A microarray of genes, or polynucleotide fragments or RNA transcripts thereof for distinguishing a neuroendocrine tumor cell, said microarray comprising a solid support having greater than 10 genes, or polynucleotide fragments or RNA transcripts thereof, distinguishably arrayed in spaced apart regions, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) cell, a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell, a typical carcinoid (TC) neuroendocrine tumor cell, or an atypical carcinoid (AC) neuroendocrine tumor cell, relative to a normal cell or a cell belonging to a different neuroendocrine tumor cell type, to permit said microarray to distinguish a neuroendocrine tumor cell.

21.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a neuroendocrine tumor cell relative to a normal cell to permit said microarray to distinguish between a neuroendocrine tumor cell and a normal cell.

22.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell to

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permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell.

23.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

24.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

25.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

26.    (original)    The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC)

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neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell
to permit said microarray to distinguish between a large cell neuroendocrine carcinoma
(LCNEC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor
cell.

27.    (original)    The microarray of claim 20, wherein said microarray comprises
a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that
are differentially expressed in a typical carcinoid (TC) neuroendocrine tumor cell relative to
an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to
distinguish between a typical carcinoid (TC) neuroendocrine tumor cell and an atypical
carcinoid (AC) neuroendocrine tumor cell.

28.    (original)    The microarray of claim 20, wherein said genes or
polynucleotide fragments or RNA transcripts thereof of said microarray include one or
more genes selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L,
CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGDIA, ARL7,
ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1,
GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB,
POLA2, POLD2, POLE3, PYCRI, SIP2-28, SIVA, SURF1, TADA3L, TK1, TYMSTR, and
VATI, or a polynucleotide fragment or RNA transcript thereof.

29.    (original)    The method of claim 28, wherein said genes or polynucleotide
fragments or RNA transcripts thereof of said microarray include one or more genes
selected from the group consisting of GGH and CPE, or a polynucleotide fragment or RNA
transcript thereof.

30.    (new)    The method of claim 1, wherein said plurality of genes includes
one or more genes selected from the group consisting of GRIA2, CPE, ORC4L, C5, GGH,
P311, NR3C1, SYNJ2, ADD3, KIM0751, PSMC6, FTHFD, DGKG, SMG1, TAF2, EIF2S1,

ZNF202, SLC24A1, FPRL1, IL6ST, ITGBL1, IL8RB, PRKM2, CSF2RB, PTK6, NPAT,
TNFRSF6, , PDGFRB, ABCG2, COL15A1, PTPN12, DMTF1, SLC22A1LS, 165393,
OXCT, PRLR, IL13RA2, MPZL1, RUNX3, S100A4, CSTF2, SNAPC4, EMP3, FLJ11560,
GBP2, DYRK3, MYO40, PNLIPRP2, SEC4L, CTAG2, LOC56311, DKFZP566B084,
FLJ20485, HNRPA0, HOXD9, JUN, 163762, VLGR1, PUM1, KRT18, CDC20, PIM1,
ATP6F, POLE3, KRT5, FEN1, SIP2-28, VATI, GUK1, SIVA, CAPG, CLDN11, IL17F,
PFKL, CTSC, ACY1, GSK3B, METTL1, CYP27B1, HMGE, WNT7A, CASP4, PTTG1,
ARF4L, CDC34, PYCR1, PGAM1, ATIC, IRAK1, DHCR7, TK1, CDKN2A, GNB1, CSTF1,
HXB, CNTN2, SSRP1, TAF12, ERP70, NP, PHB, ARL7, LIMK2, PTK9L, DDX28, SURF1,
HDAC7A, EMP1, P114-RHO-GEF, KIM0469, E2-EPF, DPH2L2, PSME3, POLA2, GALE,
APOL1, FN14, BAK1, ARHGDIA, ITPA, PDAP1, APRT, APG12L, TST, ST14, DXS1283E,
ACTG2, RIPK1, SCAMP2, COMT, POLR2D, CAPZB, POLD2, C2F, GMPPB, FARSL,
POLM, MYBPH, 163276, ERCC1, G5B, TADA3L, GNP1, MRPL49, MEN1, BAD, FKBP1A,
HSXQ28ORF, TRAP1, KIM0175, DUSP4, FRAT2, KIAA0415, NOLC1, H2AFX, RAE1,
DTX2, MAFG, FUS, LIG1, UNG, GCN1L1, REG1B, SPINT1, CAMKK2, BLM, RNUT1,
GRWD, MADH3, SNAPC2, LTBR, TACC3, PSMC4, SMARCD2, BSG, JUP, HRMT1L2,
ENTPD1, C3, YARS, ERF, TYMSTR, GS2NA, MARK3, PEX10, ANXA3, NFKBIE, HYAL2,
H4FE, TIP-1, PES1, RAE1, RFC4, TCEA2, TUBB, TIM17B, KIM0670, and RTVP1.

    31.   (new)       The method of claim 3, wherein said plurality of genes includes
one or more genes selected from the group consisting of GRIA2, CPE, ORC4L, C5, GGH,
P311, NR3C1, SYNJ2, ADD3, KIM0751, PSMC6, FTHFD, DGKG, SMG1, TAF2, EIF2S1,
ZNF202, SLC24A1, FPRL1, IL6ST, ITGBL1, IL8RB, PRKM2, CSF2RB, PTK6, NPAT,
TNFRSF6, , PDGFRB, ABCG2, COL15A1, PTPN12, DMTF1, SLC22A1LS, 165393,
OXCT, PRLR, IL13RA2, MPZL1, RUNX3, S100A4, CSTF2, SNAPC4, EMP3, FLJ11560,
GBP2, DYRK3, MYO40, PNLIPRP2, SEC4L, CTAG2, LOC56311, DKFZP566B084,
FLJ20485, HNRPA0, HOXD9, JUN, 163762, VLGR1, PUM1, KRT18, CDC20, PIM1,
ATP6F, POLE3, KRT5, FEN1, SIP2-28, VATI, GUK1, SIVA, CAPG, CLDN11, IL17F,
PFKL, CTSC, ACY1, GSK3B, METTL1, CYP27B1, HMGE, WNT7A, CASP4, PTTG1,

ARF4L, CDC34, PYCR1, PGAM1, ATIC, IRAK1, DHCR7, TK1, CDKN2A, GNB1, CSTF1,
HXB, CNTN2, SSRP1, TAF12, ERP70, NP, PHB, ARL7, LIMK2, PTK9L, DDX28, SURF1,
HDAC7A, EMP1, P114-RHO-GEF, KIM0469, E2-EPF, DPH2L2, PSME3, POLA2, GALE,
APOL1, FN14, BAK1, ARHGDIA, ITPA, PDAP1, APRT, APG12L, TST, ST14, DXS1283E,
ACTG2, RIPK1, SCAMP2, COMT, POLR2D, CAPZB, POLD2, C2F, GMPPB, FARSL,
POLM, MYBPH, 163276, ERCC1, G5B, TADA3L, GNP1, MRPL49, MEN1, BAD, FKBP1A,
HSXQ28ORF, TRAP1, KIM0175, DUSP4, FRAT2, KIAA0415, NOLC1, H2AFX, RAE1,
DTX2, MAFG, FUS, LIG1, UNG, GCN1L1, REG1B, SPINT1, CAMKK2, BLM, RNUT1,
GRWD, MADH3, SNAPC2, LTBR, TACC3, PSMC4, SMARCD2, BSG, JUP, HRMT1L2,
ENTPD1, C3, YARS, ERF, TYMSTR, GS2NA, MARK3, PEX10, ANXA3, NFKBIE, HYAL2,
H4FE, TIP-1, PES1, RAE1, RFC4, TCEA2, TUBB, TIM17B, KIM0670, and RTVP1.